



# 7

GZ 2094.00 Sequence Listing  
SEQUENCE LISTING

<110> Nicolette, Charles

<120> THERAPEUTIC ANTI-MELANOMA COMPOUNDS

<130> GZ 2094.00

<140> 09/812,238

<141> 2001-03-19

<160> 19

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 2130

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (22)...(2004)

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Met Asp Leu Val Leu Lys Arg Cys Leu Leu	10
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cat ttg gct gtg ata ggt gct ttg ctg gct gtg ggg gct aca aaa gta	99
His Leu Ala Val Ile Gly Ala Leu Leu Ala Val Gly Ala Thr Lys Val	25
15 20	
ccc aga aac cag gac tgg ctt ggt gtc tca agg caa ctc aga acc aaa	147
Pro Arg Asn Gln Asp Trp Leu Gly Val Ser Arg Gln Leu Arg Thr Lys	40
30 35	
gcc tgg aac agg cag ctg tat cca gag tgg aca gaa gcc cag aga ctt	195
Ala Trp Asn Arg Gln Leu Tyr Pro Glu Trp Thr Glu Ala Gln Arg Leu	55
45 50	
gac tgc tgg aga ggt ggt caa gtg tcc ctc aag gtc agt aat gat ggg	243
Asp Cys Trp Arg Gly Gly Gln Val Ser Leu Lys Val Ser Asn Asp Gly	70
60 65	
cct aca ctg att ggt gca aat gcc tcc ttc tct att gcc ttg aac ttc	291
Pro Thr Leu Ile Gly Ala Asn Ala Ser Phe Ser Ile Ala Leu Asn Phe	90
75 80 85	
cct gga agc caa aag gta ttg cca gat ggg cag gtt atc tgg gtc aac	339
Pro Gly Ser Gln Lys Val Leu Pro Asp Gly Gln Val Ile Trp Val Asn	105
95 100	
aat acc atc atc aat ggg agc cag gtg tgg gga gga cag cca gtg tat	387
Asn Thr Ile Ile Asn Gly Ser Gln Val Trp Gly Gly Gln Pro Val Tyr	120
110 115	
ccc cag gaa act gac gat gcc tgc atc ttc cct gat ggt gga cct tgc	435
Pro Gln Glu Thr Asp Asp Ala Cys Ile Phe Pro Asp Gly Gly Pro Cys	135
125 130	
cca tct ggc tct tgg tct cag aag aga agc ttt gtt tat gtc tgg aag	483

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Pro	Ser	Gly	Ser	Trp	Ser	Gln	Lys	Arg	Ser	Phe	Val	Tyr	Val	Trp	Lys	
140						145					150					
acc	tgg	ggc	caa	tac	tgg	caa	ggt	cta	ggg	ggc	cca	gtg	tct	ggg	ctg	531
Thr	Trp	Gly	Gln	Tyr	Trp	Gln	Val	Leu	Gly	Gly	Pro	Val	Ser	Gly	Leu	
155					160				165						170	
agc	att	ggg	aca	ggc	agg	gca	atg	ctg	ggc	aca	cac	acc	atg	gaa	gtg	579
Ser	Ile	Gly	Thr	Gly	Arg	Ala	Met	Leu	Gly	Thr	His	Thr	Met	Glu	Val	
				175					180					185		
act	gtc	tac	cat	cgc	cgg	gga	tcc	cgg	agc	tat	gtg	cct	ctt	gct	cat	627
Thr	Val	Tyr	His	Arg	Arg	Gly	Ser	Arg	Ser	Tyr	Val	Pro	Leu	Ala	His	
			190					195					200			
tcc	agc	tca	gcc	ttc	acc	att	act	gac	cag	gtg	cct	ttc	tcc	gtg	agc	675
Ser	Ser	Ser	Ala	Phe	Thr	Ile	Thr	Asp	Gln	Val	Pro	Phe	Ser	Val	Ser	
		205				210					215					
gtg	tcc	cag	ttg	cgg	gcc	ttg	gat	gga	ggg	aac	aag	cac	ttc	ctg	aga	723
Val	Ser	Gln	Leu	Arg	Ala	Leu	Asp	Gly	Gly	Asn	Lys	His	Phe	Leu	Arg	
	220					225					230					
aat	cag	cct	ctg	acc	ttt	gcc	ctc	cag	ctc	cat	gac	ccc	agt	ggc	tat	771
Asn	Gln	Pro	Leu	Thr	Phe	Ala	Leu	Gln	Leu	His	Asp	Pro	Ser	Gly	Tyr	
235					240					245					250	
ctg	gct	gaa	gct	gac	ctc	tcc	tac	acc	tgg	gac	ttt	gga	gac	agt	agt	819
Leu	Ala	Glu	Ala	Asp	Leu	Ser	Tyr	Thr	Trp	Asp	Phe	Gly	Asp	Ser	Ser	
				255					260					265		
gga	acc	ctg	atc	tct	cgg	gca	ctt	gtg	gtc	act	cat	act	tac	ctg	gag	867
Gly	Thr	Leu	Ile	Ser	Arg	Ala	Leu	Val	Val	Thr	His	Thr	Tyr	Leu	Glu	
			270					275					280			
cct	ggc	cca	gtc	act	gcc	cag	gtg	gtc	ctg	cag	gct	gcc	att	cct	ctc	915
Pro	Gly	Pro	Val	Thr	Ala	Gln	Val	Val	Leu	Gln	Ala	Ala	Ile	Pro	Leu	
		285					290				295					
acc	tcc	tgt	ggc	tcc	tcc	cca	gtt	cca	ggc	acc	aca	gat	ggg	cac	agg	963
Thr	Ser	Cys	Gly	Ser	Ser	Pro	Val	Pro	Gly	Thr	Thr	Asp	Gly	His	Arg	
	300					305					310					
cca	act	gca	gag	gcc	cct	aac	acc	aca	gct	ggc	caa	gtg	cct	act	aca	1011
Pro	Thr	Ala	Glu	Ala	Pro	Asn	Thr	Thr	Ala	Gly	Gln	Val	Pro	Thr	Thr	
					320					325					330	
gaa	gtt	gtg	ggt	act	aca	cct	ggt	cag	gcg	cca	act	gca	gag	ccc	tct	1059
Glu	Val	Val	Gly	Thr	Thr	Pro	Gly	Gln	Ala	Pro	Thr	Ala	Glu	Pro	Ser	
				335					340					345		
gga	acc	aca	tct	gtg	cag	gtg	cca	acc	act	gaa	gtc	ata	agc	act	gca	1107
Gly	Thr	Thr	Ser	Val	Gln	Val	Pro	Thr	Thr	Glu	Val	Ile	Ser	Thr	Ala	
			350					355					360			
cct	gtg	cag	atg	cca	act	gca	gag	agc	aca	ggt	atg	aca	cct	gag	aag	1155
Pro	Val	Gln	Met	Pro	Thr	Ala	Glu	Ser	Thr	Gly	Met	Thr	Pro	Glu	Lys	
		365					370					375				
gtg	cca	gtt	tca	gag	gtc	atg	ggt	acc	aca	ctg	gca	gag	atg	tca	act	1203
Val	Pro	Val	Ser	Glu	Val	Met	Gly	Thr	Thr	Leu	Ala	Glu	Met	Ser	Thr	
	380					385					390					

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cca gag gct aca ggt atg aca cct gca gag gta tca att gtg gtg ctt Pro Glu Ala Thr Gly Met Thr Pro Ala Glu Val Ser Ile Val Val Leu 395 400 405 410	1251
tct gga acc aca gct gca cag gta aca act aca gag tgg gtg gag acc Ser Gly Thr Thr Ala Ala Gln Val Thr Thr Glu Trp Val Glu Thr 415 420 425	1299
aca gct aga gag cta cct atc cct gag cct gaa ggt cca gat gcc agc Thr Ala Arg Glu Leu Pro Ile Pro Glu Pro Glu Gly Pro Asp Ala Ser 430 435 440	1347
tca atc atg tct acg gaa agt att aca ggt tcc ctg ggc ccc ctg ctg Ser Ile Met Ser Thr Glu Ser Ile Thr Gly Ser Leu Gly Pro Leu Leu 445 450 455	1395
gat ggt aca gcc acc tta agg ctg gtg aag aga caa gtc ccc ctg gat Asp Gly Thr Ala Thr Leu Arg Arg Leu Val Lys Arg Gln Val Pro Leu Asp 460 465 470	1443
tgt gtt ctg tat cga tat ggt tcc ttt tcc gtc acc ctg gac att gtc Cys Val Leu Tyr Arg Tyr Gly Ser Phe Ser Val Thr Leu Asp Ile Val 475 480 485 490	1491
cag ggt att gaa agt gcc gag atc ctg cag gct gtg ccg tcc ggt gag Gln Gly Ile Glu Ser Ala Glu Ile Leu Gln Ala Val Pro Ser Gly Glu 495 500 505	1539
ggg gat gca ttt gag ctg act gtg tcc tgc caa ggc ggg ctg ccc aag Gly Asp Ala Phe Glu Leu Thr Val Ser Cys Gln Gly Gly Leu Pro Lys 510 515 520	1587
gaa gcc tgc atg gag atc tca tcg cca ggg tgc cag ccc cct gcc cag Glu Ala Cys Met Glu Ile Ser Ser Pro Gly Cys Gln Pro Pro Ala Gln 525 530 535	1635
cgg ctg tgc cag cct gtg cta ccc agc cca gcc tgc cag ctg gtt ctg Arg Leu Cys Gln Pro Val Leu Pro Ser Pro Ala Cys Gln Leu Val Leu 540 545 550	1683
cac cag ata ctg aag ggt ggc tcg ggg aca tac tgc ctc aat gtg tct His Gln Ile Leu Lys Gly Gly Ser Gly Thr Tyr Cys Leu Asn Val Ser 555 560 565 570	1731
ctg gct gat acc aac agc ctg gca gtg gtc agc acc cag ctt atc atg Leu Ala Asp Thr Asn Ser Leu Ala Val Val Ser Thr Gln Leu Ile Met 575 580 585	1779
cct ggt caa gaa gca ggc ctt ggg cag gtt ccg ctg atc gtg ggc atc Pro Gly Gln Glu Ala Gly Leu Gly Gln Val Pro Leu Ile Val Gly Ile 590 595 600	1827
ttg ctg gtg ttg atg gct gtg gtc ctt gca tct ctg ata tat agg cgc Leu Leu Val Leu Met Ala Val Val Leu Ala Ser Leu Ile Tyr Arg Arg 605 610 615	1875
aga ctt atg aag caa gac ttc tcc gta ccc cag ttg cca cat agc agc Arg Leu Met Lys Gln Asp Phe Ser Val Pro Gln Leu Pro His Ser Ser 620 625 630	1923
agt cac tgg ctg cgt cta ccc cgc atc ttc tgc tct tgt ccc att ggt Ser His Trp Leu Arg Leu Pro Arg Ile Phe Cys Ser Cys Pro Ile Gly 635 640 645 650	1971

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gag aat agc ccc ctc ctc agt ggg cag cag gtc tgagtactct catatgatgc 2024  
 Glu Asn Ser Pro Leu Leu Ser Gly Gln Gln Val  
 655 660

tgtgattttc ctggagttga cagaaacacc tatattttccc ccagtcttcc ctgggagact 2084  
 actattaact gaaataaata ctcagagcct gaaaaaaaaa aaaaaa 2130

<210> 2  
 <211> 661  
 <212> PRT  
 <213> Homo sapiens

<400> 2  
 Met Asp Leu Val Leu Lys Arg Cys Leu Leu His Leu Ala Val Ile Gly  
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 Ala Leu Leu Ala Val Gly Ala Thr Lys Val Pro Arg Asn Gln Asp Trp  
 20 25 30  
 Leu Gly Val Ser Arg Gln Leu Arg Thr Lys Ala Trp Asn Arg Gln Leu  
 35 40 45  
 Tyr Pro Glu Trp Thr Glu Ala Gln Arg Leu Asp Cys Trp Arg Gly Gly  
 50 55 60  
 Gln Val Ser Leu Lys Val Ser Asn Asp Gly Pro Thr Leu Ile Gly Ala  
 65 70 75 80  
 Asn Ala Ser Phe Ser Ile Ala Leu Asn Phe Pro Gly Ser Gln Lys Val  
 85 90 95  
 Leu Pro Asp Gly Gln Val Ile Trp Val Asn Asn Thr Ile Ile Asn Gly  
 100 105 110  
 Ser Gln Val Trp Gly Gly Gln Pro Val Tyr Pro Gln Glu Thr Asp Asp  
 115 120 125  
 Ala Cys Ile Phe Pro Asp Gly Gly Pro Cys Pro Ser Gly Ser Trp Ser  
 130 135 140  
 Gln Lys Arg Ser Phe Val Tyr Val Trp Lys Thr Trp Gly Gln Tyr Trp  
 145 150 155 160  
 Gln Val Leu Gly Gly Pro Val Ser Gly Leu Ser Ile Gly Thr Gly Arg  
 165 170 175  
 Ala Met Leu Gly Thr His Thr Met Glu Val Thr Val Tyr His Arg Arg  
 180 185 190  
 Gly Ser Arg Ser Tyr Val Pro Leu Ala His Ser Ser Ser Ala Phe Thr  
 195 200 205  
 Ile Thr Asp Gln Val Pro Phe Ser Val Ser Val Ser Gln Leu Arg Ala  
 210 215 220  
 Leu Asp Gly Gly Asn Lys His Phe Leu Arg Asn Gln Pro Leu Thr Phe  
 225 230 235 240  
 Ala Leu Gln Leu His Asp Pro Ser Gly Tyr Leu Ala Glu Ala Asp Leu  
 245 250 255  
 Ser Tyr Thr Trp Asp Phe Gly Asp Ser Ser Gly Thr Leu Ile Ser Arg  
 260 265 270  
 Ala Leu Val Val Thr His Thr Tyr Leu Glu Pro Gly Pro Val Thr Ala  
 275 280 285  
 Gln Val Val Leu Gln Ala Ala Ile Pro Leu Thr Ser Cys Gly Ser Ser  
 290 295 300  
 Pro Val Pro Gly Thr Thr Asp Gly His Arg Pro Thr Ala Glu Ala Pro  
 305 310 315 320  
 Asn Thr Thr Ala Gly Gln Val Pro Thr Thr Glu Val Val Gly Thr Thr  
 325 330 335  
 Pro Gly Gln Ala Pro Thr Ala Glu Pro Ser Gly Thr Thr Ser Val Gln  
 340 345 350  
 Val Pro Thr Thr Glu Val Ile Ser Thr Ala Pro Val Gln Met Pro Thr  
 355 360 365  
 Ala Glu Ser Thr Gly Met Thr Pro Glu Lys Val Pro Val Ser Glu Val  
 370 375 380  
 Met Gly Thr Thr Leu Ala Glu Met Ser Thr Pro Glu Ala Thr Gly Met

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385          390          395          400
Thr Pro Ala Glu Val Ser Ile Val Val Leu Ser Gly Thr Thr Ala Ala
Gln Val Thr Thr Thr Glu Trp Val Glu Thr Thr Ala Arg Glu Leu Pro
Ile Pro Glu 420 Glu Gly Pro Asp Ala Ser Ser Ile Met Ser Thr Glu
Ser Ile Thr Gly Ser Leu Gly Pro Leu Leu Asp Gly Thr Ala Thr Leu
Arg Leu Val Lys Arg Gln Val Pro Leu Asp Cys Val Leu Tyr Arg Tyr
Gly Ser Phe Ser Val Thr Leu Asp Ile Val Gln Gly Ile Glu Ser Ala
Glu Ile Leu Gln Ala Val Pro Ser Gly Glu Gly Asp Ala Phe Glu Leu
Thr Val Ser Cys Gln Gly Gly Leu Pro Lys Glu Ala Cys Met Glu Ile
Ser Ser Pro Gly Cys Gln Pro Pro Ala Gln Arg Leu Cys Gln Pro Val
Leu Pro Ser Pro Ala Cys Gln Leu Val Leu His Gln Ile Leu Lys Gly
Gly Ser Gly Thr Tyr Cys Leu Asn Val Ser Leu Ala Asp Thr Asn Ser
Leu Ala Val Val Ser Thr Gln Leu Ile Met Pro Gly Gln Glu Ala Gly
Leu Gly Gln Val Pro Leu Ile Val Gly Ile Leu Leu Val Leu Met Ala
Val Val Leu Ala Ser Leu Ile Tyr Arg Arg Arg Leu Met Lys Gln Asp
Phe Ser Val Pro Gln Leu Pro His Ser Ser Ser His Trp Leu Arg Leu
Pro Arg Ile Phe Cys Ser Cys Pro Ile Gly Glu Asn Ser Pro Leu Leu
Ser Gly Gln Gln Val

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<210> 3  
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 <212> PRT  
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 Ser Phe Asp Gln Val Pro Phe Ser Val  
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<210> 4  
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 <222> 3, 15, 18, 24, 27  
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<210> 5  
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<223> n= A, T, C or G

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<210> 11  
<211> 9

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 <400> 11  
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<400> 13  
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 <223> n= A, T, C or G

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<210> 15  
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<400> 15  
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 <223> n= A, T, C or G

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 <212> PRT  
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<400> 17  
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<210> 18  
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<400> 19  
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 1 5